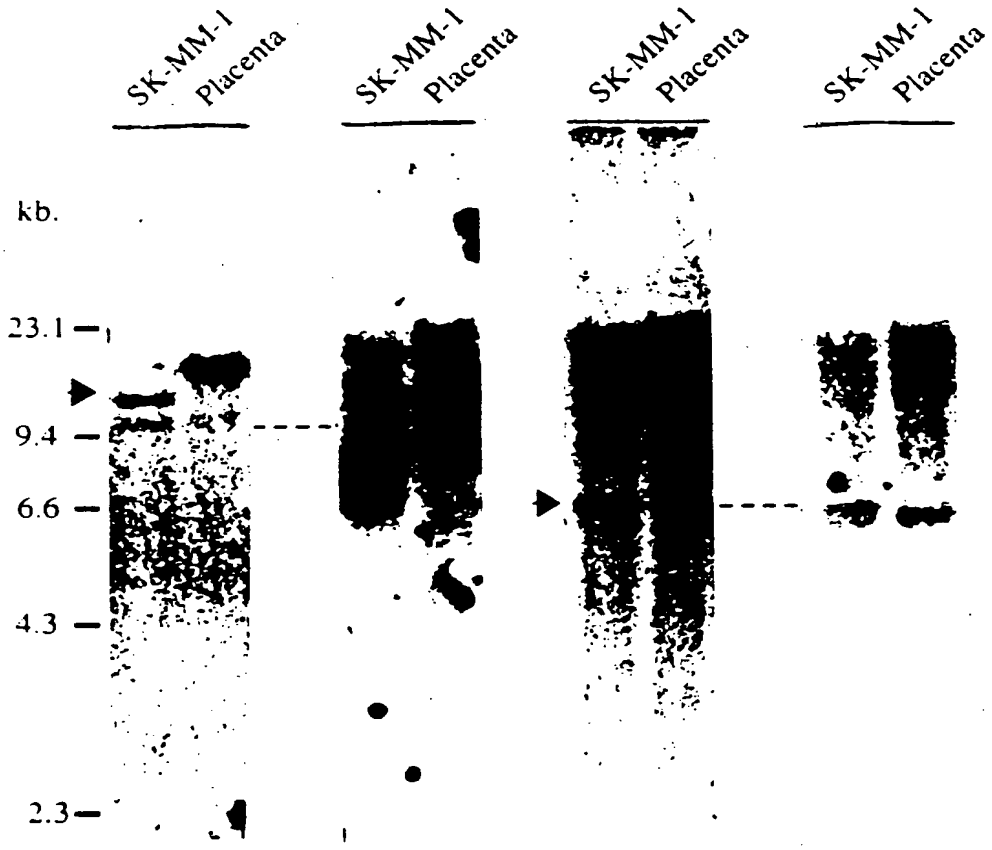
FIG. 1


SK-MM-1
Placenta
SK-MM-1
Placenta
SK-MM-1
Placenta
SK-MM-1
Placenta
kb.
23.1
9.4
6.6
4.3
2.3
JH
Cγ2
Cμ
0.7B/H

*Bam*HI

FIG. 2A

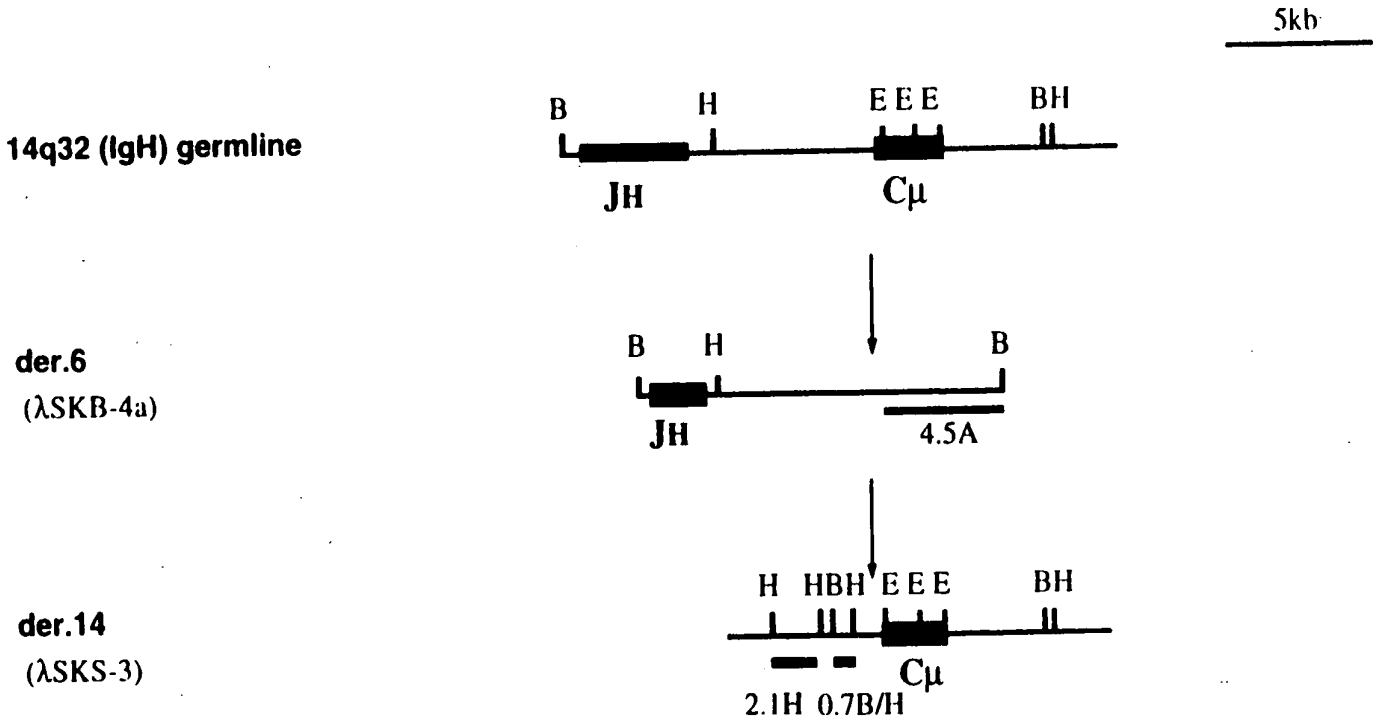


FIG. 2B

```
.6   TTTTCTCTCTACAGTCACCTCCCTGTTTACCAAAGATAATCACAATAAGTCCAGTTTACTTACAAAACAAGTTTAGT
                                                   |||||||||||||||||||||||||||||||
.6   TGGGCTCGGCC-TGGTGGGGCAGCCACAGCGGACGC-AGTAGTGAAAGTCCAGTTTACTTACAAAACAAGTTTAGT
     ||||||||||| ||||||||||||||||||||||||| ||||||||
14   TGGGCTCGGCCTTGGTGGGGCAGCCACAGCGGACGCAAGTAGTGAGGGCACTCAGAACGCCACTCAGCCCCGACAG
        4400      4410      4420      4430      4440      4450      4460      4470

.6   TATTAGAGGAAACTAAAACTTCAGGATTCAGTCCAGATAATTTTTAAAAACTCTAAAACAATGGACAGGGCTAGAAT
     ||||||||||||||||||||||||||||||
.14  TATTAGAGGAAACTAAAACTTCAGGATTCAGCAGGGCATGAGGAGGCAGCTCCTCACCCTCCCTTTCTCTTTTGTAC
                                   |||||||| |||||||||||||||||||||||||||||||||||
.14  GGCACTCAGAACGCCACTCAGCCCCGACAGGCAGGGCACGAGGAGGCAGCTCCTCACCCTCCCTTTCTCTTTTGT--
        4450      4460      4470      4480      4490      4500      4510
```

FIG. 3A

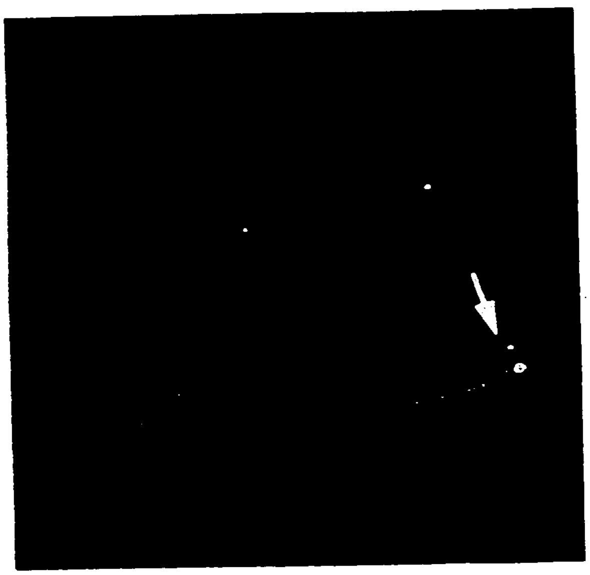


FIG. 3B

λMUM-3

FIG. 4A

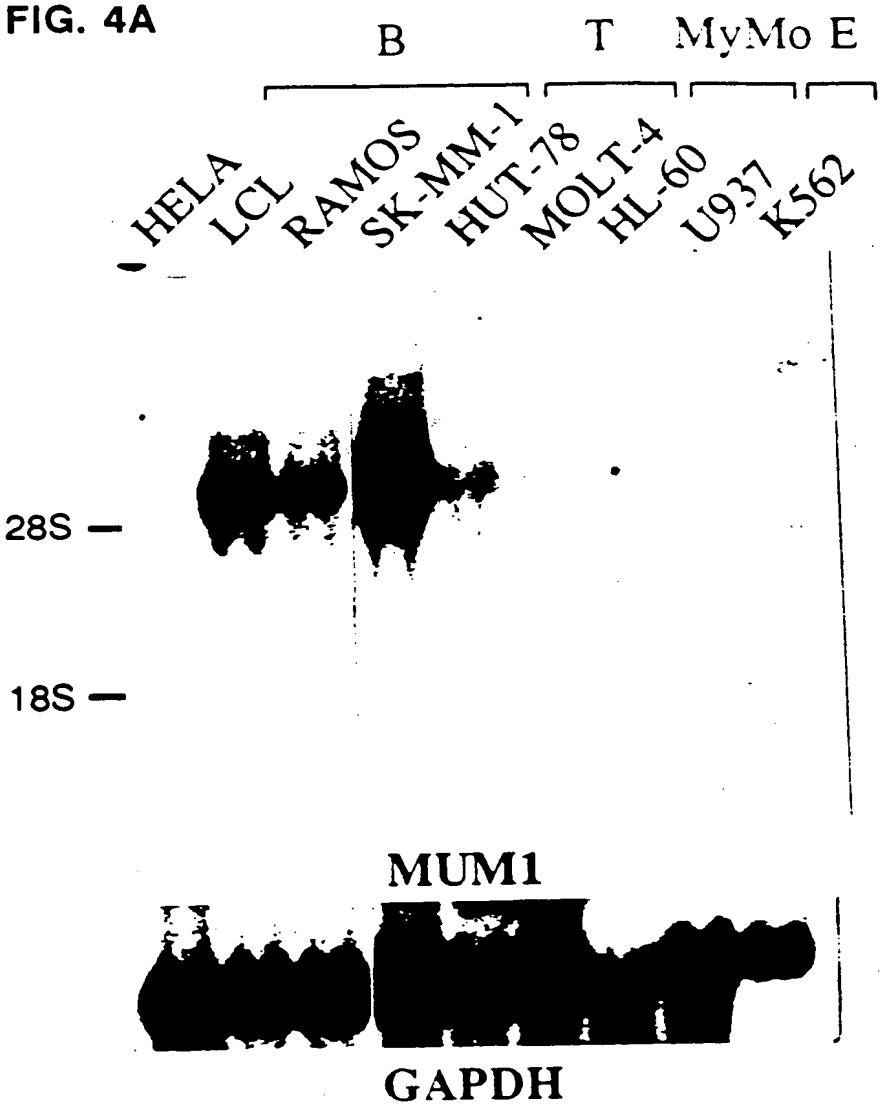

B
T
MyMo
E
HELA
LCL
RAMOS
SK-MM-1
HUT-78
MOLT-4
HL-60
U937
K562
28S
18S
MUM1
GAPDH

FIG. 4B

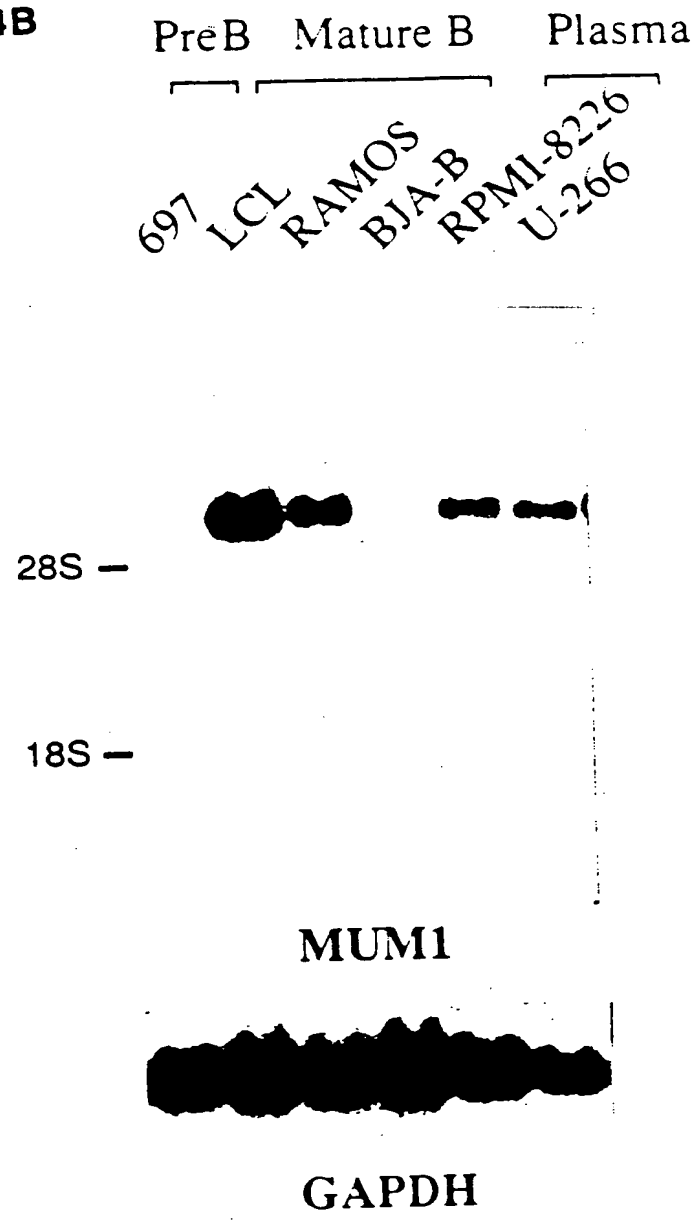

PreB
Mature B
Plasma
697
LCL
RAMOS
BJA-B
RPMI-8226
U-266
28S
18S
MUM1
GAPDH

FIG. 4C

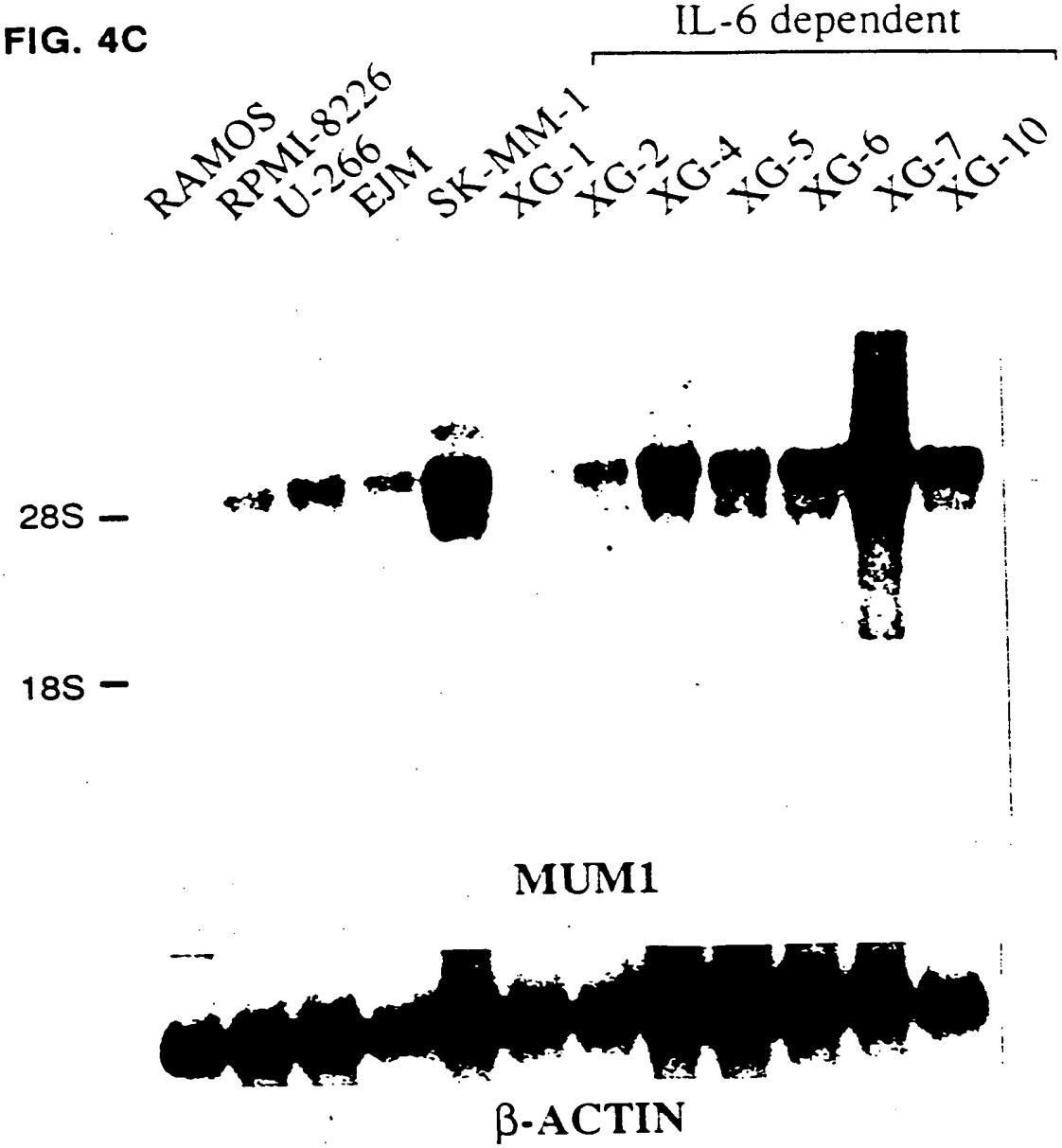

IL-6 dependent
RAMOS
RPMI-8226
U-266
EJM
SK-MM-1
XG-1
XG-2
XG-4
XG-5
XG-6
XG-7
XG-10
28S
18S
MUM1
β-ACTIN

FIG. 5A

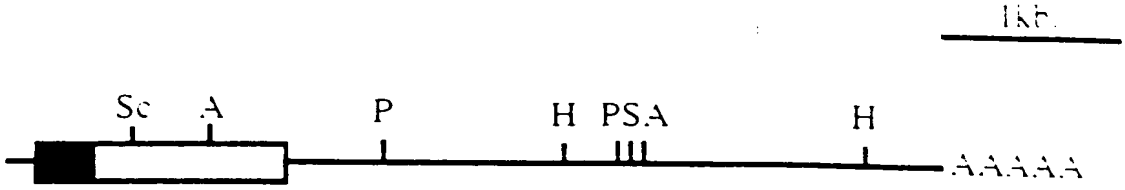


FIG. 5B-1

```
   1  GCCTGACCAA CATGGTAAAA CCCCATCTCT GCTAAAACTA CAAAAAAT
  51  GCTGGATGTG GTGGCAGGGA ACCTGTCATC CCAGCTAGTT GGGAGACT
 101  GGCAGGAGAA TCGCTCGATC TTGGGACCCA CCGCTGCCCT CAGCTCCG
 151  TCCAGGGCGA GTGCAGAGCA CAGCGGGCGG AGGACCCCGG GCGCGGGC
 201  GGACGGCACG CGGGGCATGA ACCTGGAGGG CGGCGGCCGA GGCGGAGA
                          M  N   L  E  G   G  G  R   G  G  E
 251  TCGGCATGAG CGCGGTGAGC TGCGGCAACG GGAAGCTCCG CCAGTGGC
        G  M  S   A  V  S   C  G  N  G   K  L  R   Q  W  L
 301  ATCGACCAGA TCGACAGCGG CAAGTACCCC GGGCTGGTGT GGGAGAAC
      I  D  Q  I   D  S  G   K  Y  P   G  L  V  W   E  N
 351  GGAGAAGAGC ATCTTCCGCA TCCCCTGGAA GCACGCGGGC AAGCAGGA
        E  K  S   I  F  R  I   P  W  K   H  A  G   K  Q  D
 401  ACAACCGCGA GGAGGACGCC GCGCTCTTCA AGGCTTGGGC ACTGTTTA
        N  R  E   E  D  A   A  L  F  K   A  W  A   L  F  K
 451  GGAAAGTTCC GAGAAGGCAT CGACAAGCCG GACCCTCCCA CCTGGAAG
        G  K  F  R   E  G  I   D  K  P   D  P  P  T   W  K
 501  GCGCCTGCGG TGCGCTTTGA ACAAGAGCAA TGACTTTGAG GAACTGGT
        R  L  R   C  A  L  N   K  S  N   D  F  E   E  L  V
 551  AGCGGAGCCA GCTGGACATC TCAGACCCGT ACAAAGTGTA CAGGATTG
        R  S  Q   L  D  I   S  D  P  Y   K  V  Y   R  I  V
 601  CCTGAGGGAG CCAAAAAAGG AGCCAAGCAG CTCACCCTGG AGGACCCG
        P  E  G  A   K  K  G   A  K  Q   L  T  L  E   D  P
 651  GATGTCCATG AGCCACCCCT ACACCATGAC AACGCCTTAC CCTTCGCT
        M  S  M   S  H  P  Y   T  M  T   T  P  Y   P  S  L
 701  CAGCCCAGCA GGTTCACAAC TACATGATGC CACCCCTCGA CCGAAGCT
        A  Q  Q   V  H  N   Y  M  M  P   P  L  D   R  S  W
 751  AGGGACTACG TCCCGGATCA GCCACACCCG GAAATCCCGT ACCAATGT
        R  D  Y  V   P  D  Q   P  H  P   E  I  P  Y   Q  C
 801  CATGACGTTT GGACCCCGCG GCCACCACTG GCAAGGCCCA GCTTGTGA
        M  T  F   G  P  R  G   H  H  W   Q  G  P   A  C  E
 851  ATGGTTGCCA GGTGACAGGA ACCTTTTATG CTTGTGCCCC ACCTGAGT
        G  C  Q   V  T  G   T  F  Y  A   C  A  P   P  E  S
 901  CAGGCTCCCG GAGTCCCCAC AGAGCCAAGC ATAAGGTCTG CCGAAGCC
        Q  A  P  G   V  P  T   E  P  S   I  R  S  A   E  A
 951  GGCGTTCTCA GACTGCCGGC TGCACATCTG CCTGTACTAC CGGGAAAT
        A  F  S   D  C  R  L   H  I  C   L  Y  Y   R  E  I
1001  TCGTGAAGGA GCTGACCACG TCCAGCCCCG AGGGCTGCCG GATCTCCC
        V  K  E   L  T  T   S  S  P  E   G  C  R   I  S  P
1051  GGACATACGT ATGACGCCAG CAACCTGGAC CAGGTCCTGT TCCCCTAC
        G  H  T  Y   D  A  S   N  L  D   Q  V  L  F   P  Y
1101  AGAGGACAAT GGCCACAGGA AAAACATTGA GAACCTGCTG AGCCACCT
        E  D  N   G  H  R  K   N  I  E   N  L  L   S  H  L
```

FIG. 5B-2

```
1151  AGAGGGGCGT GGTCCTCTGG ATGGCCCCCG ACGGGCTCTA TGCGAAAAC
        R  G  V    V  L  W    M  A  P  D    G  L  Y    A  K  R
1201  CTGTGCCAGA GCACGATCTA CTGGGACGGG CCCCTGGCGC TGTGCAACC
        L  C  Q  S    T  I  Y    W  D  G    P  L  A  L    C  N  I
1251  CCGGCCCAAC AAACTGGAGA GAGACCAGAC CTGCAAGCTC TTTGACACA
        R  P  N    K  L  E  R    D  Q  T    C  K  L    F  D  T
1301  AGCAGTTCTT GTCAGAGCTG CAAGCGTTTG CTCACCACGG CCGCTCCC
        Q  F  L    S  E  L    Q  A  F  A    H  H  G    R  S  L
1351  CCAAGATTCC AGGTGACTCT ATGCTTTGGA GAGGAGTTTC CAGACCCT
        P  R  F  Q    V  T  L    C  F  G    E  E  F  P    D  P
1401  GAGGCAAAGA AAGCTCATCA CAGCTCACGT AGAACCTCTG CTAGCCAG
        R  Q  R    K  L  I  T    A  H  V    E  P  L    L  A  R
1451  AACTATATTA TTTTGCTCAA CAAAACAGTG GACATTTCCT GAGGGGCT
        L  Y  Y    F  A  Q    Q  N  S  G    H  F  L    E  G  Y
1501  GATTTACCAG AACACATCAG CAATCCAGAA GATTACCACA GATCTATC
        D  L  P  E    H  I  S    N  P  E    D  Y  H  R    S  I
1551  CCATTCCTCT ATTCAAGAAT GAAAAATGTC AAGATGAGTG GTTTTCTT
        H  S  S    I  Q  E  *
1601  TCCTTTTTTT TTTTTTTTTT TTTGATACGG AGATACGGGG TCTTGCTC
1651  TCTCCCAGGC TGGAGTGCAG TGACACAATC TCAGCTCACT GTGACCTC
1701  CCTCCTGGGT TCAAGAGACT CTCCTGCCTC AGCCTCCCTG GTAGCTGG
1751  TTACAGGTGT GAGCCACTGC ACCCACCCAA GACAAGTGAT TTTCATTG
1801  AATATTTGAC TTTAGTGAAA GCGTCCAATT GACTGCCCTC TTACTGTT
1851  GAGGAACTCA GAAGTGGAGA TTTCAGTTCA GCGGTTGAGG AGAATTGC
1901  CGAGACAAGC ATGGAAAATC AGTGACATCT GATTGGCAGA TGAGCTTA
1951  TCAAAAGGAA GGGTGGCTTT GCATTTTCTT GTGTTCTGTA GACTGCCA
2001  ATTGATGATC ACTGTGAAAA TTGACCAAGT GATGTGTTTA CATTTACT
2051  AATGCGCTCT TTAATTTGTT GTAGATTAGG TCTTGCTGGA AGACAGAG
2101  AACTTGCCTT TCAGTATTGA CACTGACTAG AGTGATGACT GCTTGTAG
2151  ATGTCTGTGC CATTTCTCAG GGAAGTAAGA TGTAAATTGA AGAAGCCT
2201  CACGTAAAAG AAATGTATTA ATGTATGTAG GAGCTGCAGT TCTTGTGG
2251  GACACTTGCT GAGTGAAGGA AATGAATCTT TGACTGAAGC CGTGCCTG
2301  GCCTTGGGGA GGCCCATCCC CCACCTGCCA GCGGTTTCCT GGTGTGGG
2351  CCTCTGCCCC ACCCTCCTTC CCATTGGCTT TCTCTCCTTG GCCTTTCC
2401  GAAGCCAGTT AGTAAACTTC CTATTTTCTT GAGTCAAAAA ACATGAGC
2451  TACTCTTGGA TGGGACATTT TTGTCTGTCC TACAATCTAG TAATGTCT
2501  GTAATGGTTA AGTTTTCTTG TTTCTGCATC TTTTTGACCC TCATTCTT
2551  GAGATGCTAA AATTCTTCGC ATAAAGAAGA AGAAATTAAG GAACATAA
2601  CTTAATACTT GAACTGTTGC CCTTCTGTCC AAGTACTTAA CTATCTGT
2651  CCTTCCTCTG TGCCACGCTC CTCTGTTTGT TTGGCTGTCC AGCGATCA
2701  CATGGCGACA CTAAAGGAGG AGGAGCCGGG GACTCCCAGG CTGGAGAG
2751  CTGCCAGGAC CCACCACTGG AAGCAGGATG GAGCTGACTA CGGAACTG
2801  CACTCAGTGG GCTGTTTCTG CTTATTTCAT CTGTTCTATG CTTCCTCG
2851  CCAATTATAG TTTGACAGGG CCTTAAAATT ACTTGGCTTT TTCCAAAT
2901  TTCTATTTAT AGAAATCCCA AAGACCTCCA CTTGCTTAAG TATACCTA
2951  ACTTACATTT TTGTGGTTTT GAGAAAGTAC AGCAGTAGAC TGGGGCGT
```

FIG. 5B-3

3051	TCAGCAGAAG	ATTGCGTTAG	CTCTCAAATG	TGTGTTCCTG	CTTTTCT
3101	GGATATTTTA	AATTCATTCA	ACAAGCACCT	AGTAAGTGCC	TGCTGTA
3151	CTACATTACA	CAGTTCAGCC	TTTATCAAGC	TTAGTGAGCA	GTGAGCA
3201	AAACATTATT	TTTTAATGTT	TAAAAAGTTT	CTAATATTAA	AGTCAGA
3251	TTAATACAAT	TAATATTAAT	ATTAACTACA	GAAAAGACAA	ACAGTAG
3301	ACAGCAAAAA	AATAAAAAGG	ATCTCCTTTT	TTCCCAGCCC	AAATTCT
3351	CTCTAAAAGT	GTCCACAAGA	AGGGGTGTTT	ATTCTTCCAA	CACATTT
3401	TTTTCTGTAA	ATATACATAA	ACTTAAAAAG	AAAACCTCAT	GGAGTCA
3451	TGCACACACT	TTTCATGCAG	TGCTCTTTGT	AGCTAAACAG	TGAAGAT
3501	CCTCGTTCTG	CTCAGAGGCC	TTGCTGTGGA	GCTCCACTGC	CATGTAC
3551	GTAGGGTTTG	ACATTTCATT	AGCCATGCAA	CATGGATATG	TATTGGG
3601	CAGACTGTGT	TTCGTGAACT	GCAGTGATGT	ATACATCTTA	TAGATGC
3651	GTATTTTGGG	GTATATTATC	CTAAGGGAAG	ATAAAGATGA	TATTAAG
3701	TGCTGTTTCA	CGGGGCCCTT	ACCTGTGACC	CTCTTTGCTG	AAGAATA
3751	AACCCCACAC	AGCACTTCAA	AGAAGCTGTC	TTGGAAGTCT	GTCTCAG
3801	CACCCTGTCT	TCTTAATTCT	CCAAGCGGAT	GCTCCATTTC	AATTGCT
3851	TGACTTCTTC	TTCTTTGTTT	TTTTAAATAT	TATGCTGCTT	TAACAGT
3901	GCTGAATTTT	CTGGAAAATG	CTTCTTGGCT	GGGGCCACTA	CCTCCTT
3951	TATCTTTACA	TCTATGTGTA	TGTTGACTTT	TTAAAATTCT	GAGTGAT
4001	GGGTATGACC	TAGGGAATGA	ACTAGCTATG	GAAATAACTC	AGGGTTA
4051	ATCCTAGCAC	TTGTCTCAGG	ACTCTGAAAA	GGAACGGCTT	CCTCATT
4101	TGTCTTGATA	AAGTGGAATT	GGCAAACTAG	AATTTAGTTT	GTACTCA
4151	GACAGTGCTG	TTGAAGATTT	GAGGACTTGT	TAAAGAGCAC	TGGGTCA
4201	GGAAAAAATG	TATGTGTCTC	CCCAGGTGCA	TTTTCTTGGT	TTATGTC
4251	TTCTTGAGAT	TTTGTATATT	TAGGAAAACC	TCAAGCAGTA	ATTAATA
4301	CCTGGAACAC	TATAGAGAAC	CAAGTGACCG	ACTCATTTAC	AACTGAA
4351	TAGGAAGCCC	CTGAGTCCTG	AGCGAAAACA	GGAGAGTTAG	TCGCCCT
4401	GAAAACCCAG	CTAGACTATT	GGGTATGAAC	TAAAAAGAGA	CTGTGCC
4451	GTGAGAAAAA	TGTAAAATCC	TACAGTGGAA	TGAGCAGCCC	TTACAGT
4501	GTTACCACCA	AGGGCAGGTA	GGTATTAGTG	TTTGAAAAAG	CTGGTCT
4551	AGCGAGGGCA	TAAATACAGC	TAGCCCCAGG	GGTGGAACAA	CTGTGGA
4601	CTTGGGTACT	CGCACCTCTT	GGCTTTGTTG	ATGCTCCGCC	AGGAAGG
4651	CTTGTGTGTG	CGTGTCAGTT	ACTTTTTTAG	TAACAATTCA	GATCCAG
4701	AAACTTCCGT	TCATTGCTCT	CCAGTCACAT	GCCCCCACTT	CCCCACA
4751	GAAAGTTTTT	CTGAAGTGTT	GGGATTGGTT	AAGGTCTTTA	TTTGTATTA
4801	GTATCTCCCC	AAGTCCTCTG	TGGCCAGCTG	CATCTGTCTG	AATGGTGC
4851	GAAGGCTCTC	AGACCTTACA	CACCATTTTG	TAAGTTATGT	TTTACATGC
4901	CCGTTTTTGA	GACTGATCTC	GATGCAGGTG	GATCTCCTTG	AGATCCTGA
4951	AGCCTGTTAC	AGGAATGAAG	TAAAGGTCAG	TTTTTTTTGT	ATTGATTTT
5001	ACAGCTTTGA	GGAACATGCA	TAAGAAATGT	AGCTGAAGTA	GAGGGGACG
5051	GAGAGAAGGG	CCAGGCCGGC	AGGCCAACCC	TCCTCCAATG	GAAATTCCC
5101	TGTTGCTTCA	AACTGAGACA	GATGGGACTT	AACAGGCAAT	GGGGTCCAC
5151	TCCCCCTCTT	CAGCATCCCC	CGTACC		

FIG. 6A

```
MUM-1    (23-72)   KLRQWLIDQI DSGKYPGLVW ENEEKSIFRI PWKHAGKQDY NREEDAALFK
LSIRF    (23-72)   KLRQWLIDQI DSGKYPGLVW ENEEKSVFRI PWKHAGKQDY NREEDAALFK
IRF-1    (7-56)    RMRPWLEMQI NSNQIPGLIW INKEEMIFQI PWKHAAKHGW DINKDACLFR
IRF-2    (7-56)    RMRPWLEEQI NSNTIPGLKW LNKEKKIFQI PWMHAARHGW DVEKDAPLFR
ICSBP    (9-60)    RLRQWLIEQI DSSMYPGLIW ENEEKSMFRI PWKHAGKQDY NQEVDASIFK
ISGF3γ   (11-60)   KLRNWVVEQV ESGQFPGVCW DDTAKTMFRI PWKHAGKQDF REDQDAAFFK
IRF-3    (7-55)    RILPWLVSQL DLGQLEGVAW VNKSRTRFRI PWKHGLRQD. AQQEDFGIFQ

MUM-1    (73-122)  AWALFKGKFR EGIDKPDPPT WKTRLRCALN KSNDFEELVE RSQLDISDPY
LSIRF    (73-122)  AWALFKGKFR EGIDKPDPPT WKTRLRCALN KSNDFEELVE RSQLDISDPY
IRF-1    (57-106)  SWAIHTGRYK AGEKEPDPKT WKANFRCAMN SLPDIEEVKD QSRNKGSSAV
IRF-2    (57-106)  NWAIHTGKHQ PGVDKPDPKT WKANFRCAMN SLPDIEEVKD KSIKKGNNAF
ICSBP    (59-107)  AWAVFKGKFK EG.DKAEPAT WKTRLRCALN KSPDFEEVTD RSQLDISEPY
ISGF3γ   (61-109)  AWAIFKGKYK EG.DTGGPAV WKTRLRCALN KSSEFKEVPE RGRMDVAEPY
IRF-3    (56-104)  AWAEATGAYV PGRDKPDLPT WKRNFRSALN RKEGLRLAED RSK.DPHDPH

MUM-1    (123-130) KVYRIVPE
LSIRF    (123-130) KVYRIVPE
IRF-1    (107-114) RVYRMLPP
IRF-2    (107-114) RVYRMLPL
ICSBP    (108-115) KVYRIVPE
ISGF3γ   (110-117) KVYQLLPP
IRF-3    (105-112) KIYEFVNS
```

FIG. 6B

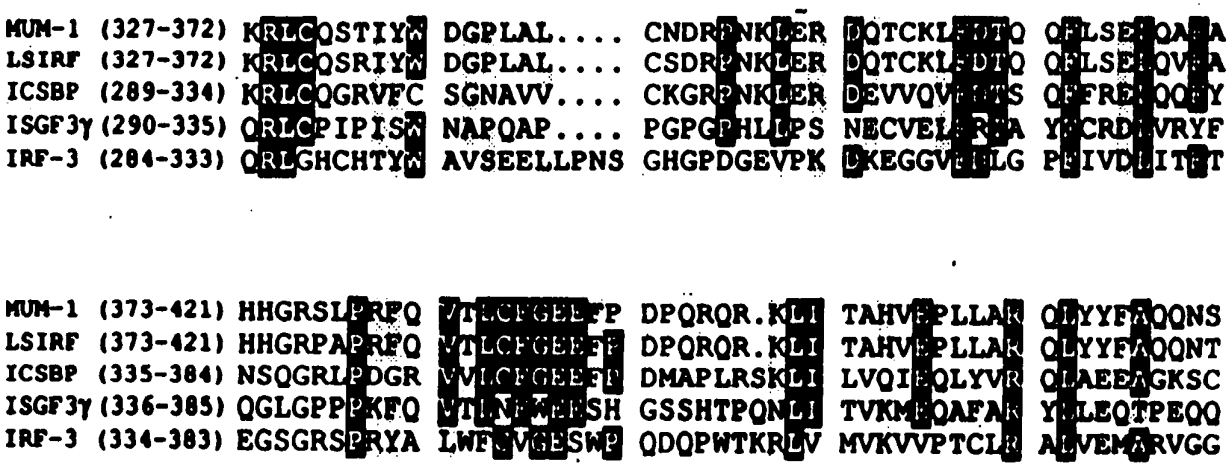
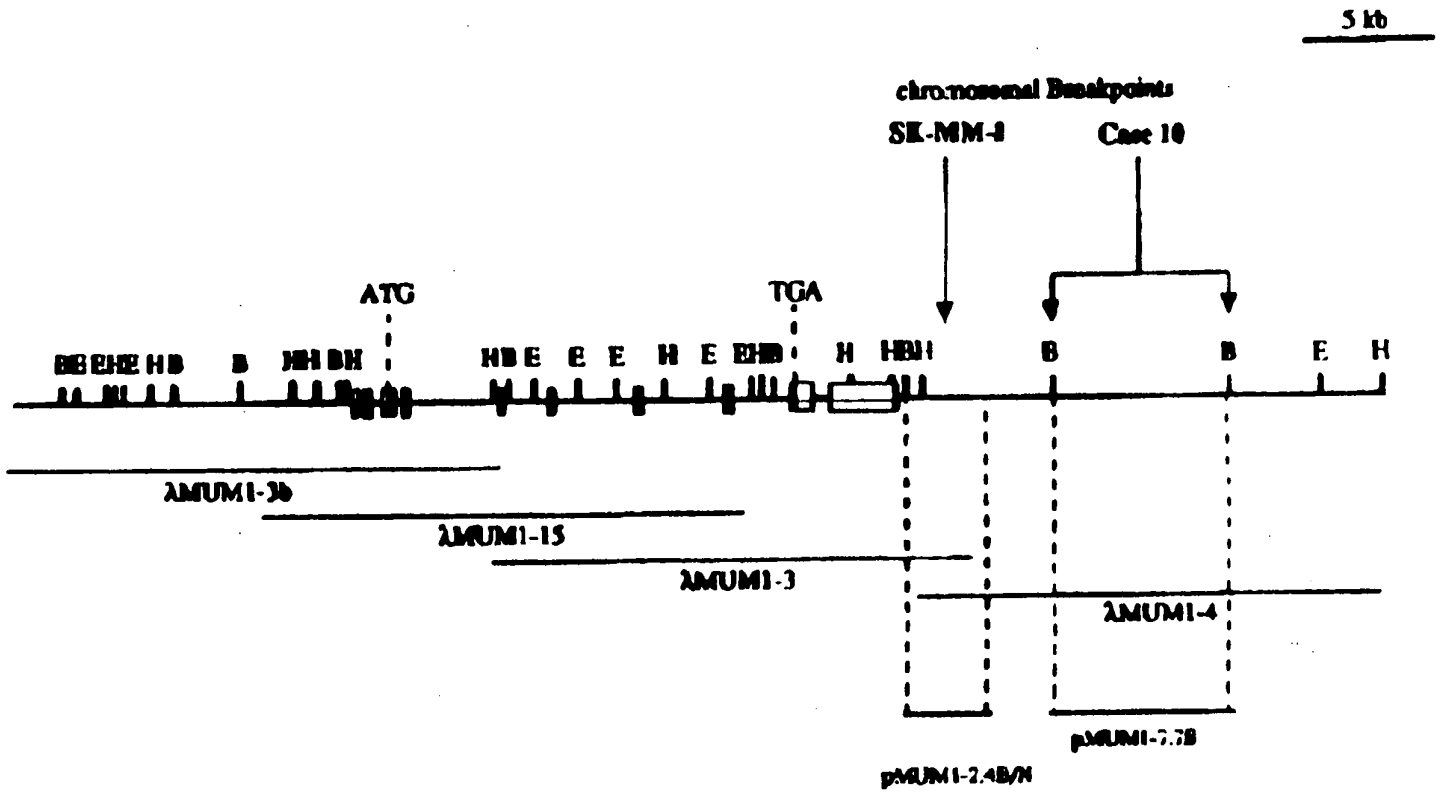

MUM-1 (327-372) KRLCQSTIYW DGPLAL.... CNDRPNKLER DQTCKLSDTQ QFLSEMQAMA
LSIRF (327-372) KRLCQSRIYW DGPLAL.... CSDRPNKLER DQTCKLSDTQ QFLSEMQVMA
ICSBP (289-334) KRLCQGRVFC SGNAVV.... CKGRPNKLER DEVVQVMTTS QFFREMQQTY
ISGF3γ (290-335) QRLCPIPISW NAPQAP.... PGPGPHLLPS NECVELMRMA YMCRDMVRYF
IRF-3 (284-333) QRLGHCHTYW AVSEELLPNS GHGPDGEVPK DKEGGVMLLG PMIVDLITMT
MUM-1 (373-421) HHGRSLPRFQ VTLCFGEEFP DPQRQR.KLI TAHVMPLLAR QLYYFAQQNS
LSIRF (373-421) HHGRPAPRFQ VTLCFGEEFP DPQRQR.KLI TAHVMPLLAR QLYYFAQQNT
ICSBP (335-384) NSQGRLPDGR VVLCFGEEFT DMAPLRSKLI LVQIMQLYVR QLAEEAGKSC
ISGF3γ (336-385) QGLGPPPKFQ VTLNFGEESH GSSHTPQNLI TVKMMQAFAK YLLEQTPEQQ
IRF-3 (334-383) EGSGRSPRYA LWFSVGESWP QDQPWTKRLV MVKVVPTCLR ALVEMARVGG

FIG. 7

Genomic locus spanning MUM1 gene



pMUM1- 7.7 B means the 7.7kb insert is BamHI sites .

B/N means BamHI/NotI site is used for cloning.
Every genomic inserts is cloned into pBluescript KS.

FIG. 8

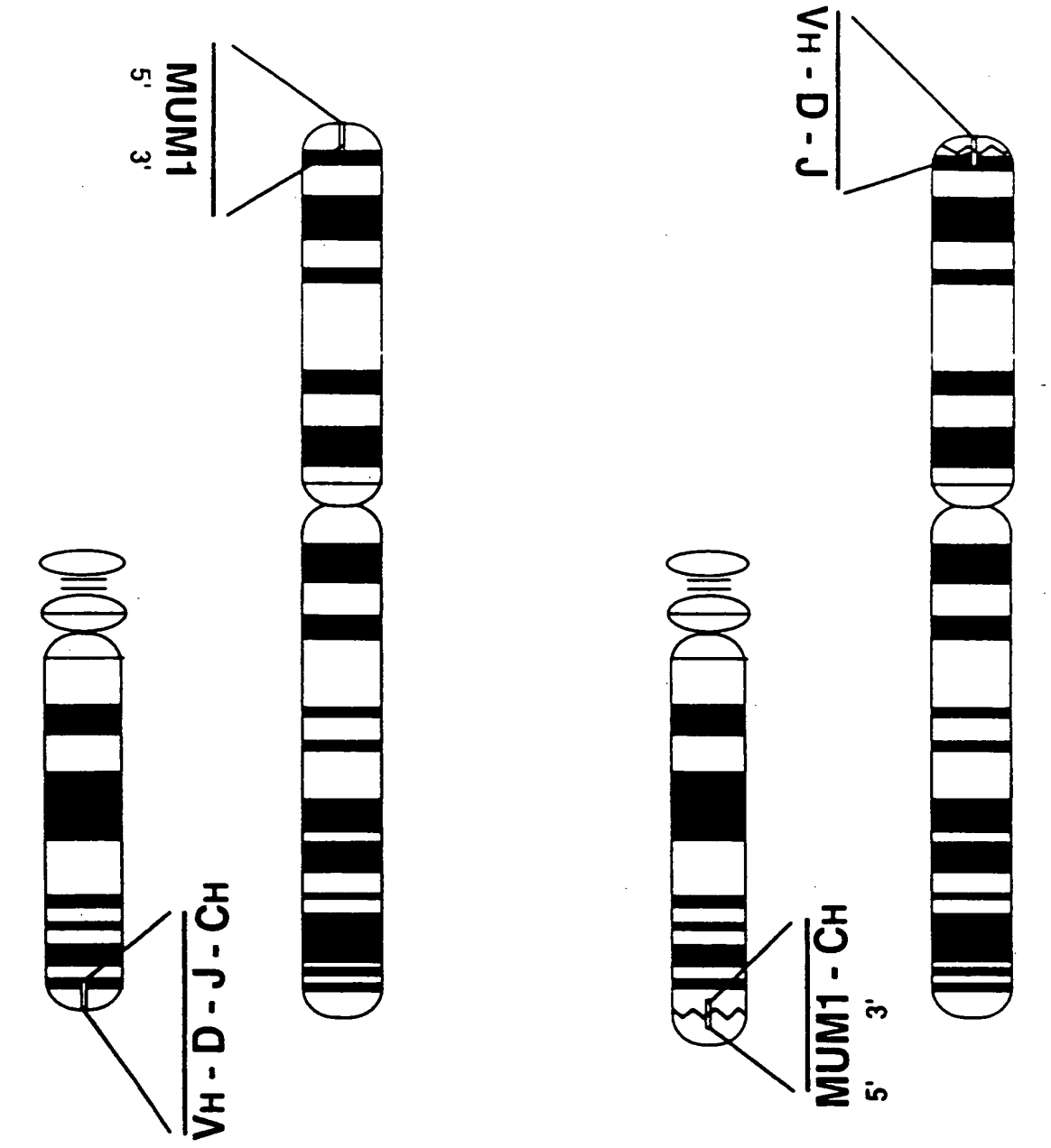


FIG. 9A

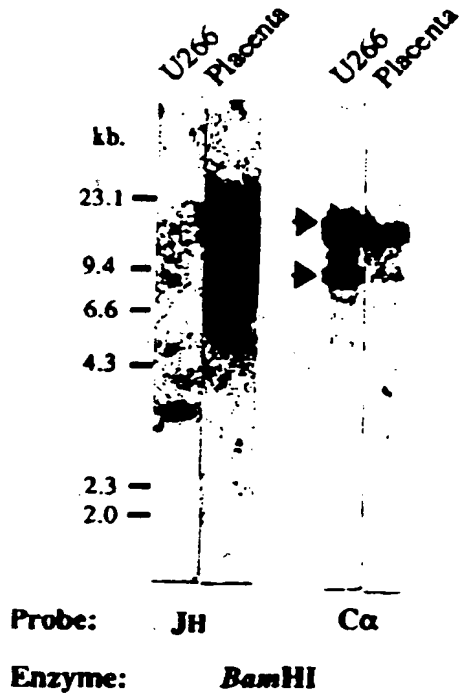
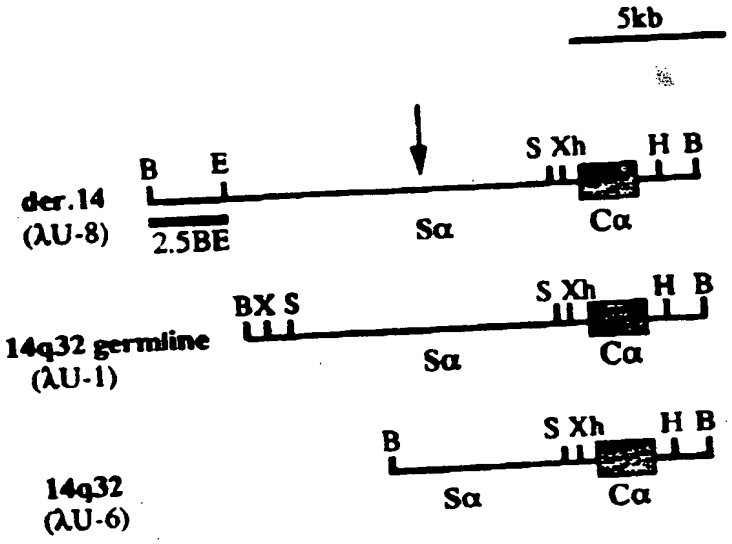

U266
Placenta
U266
Placenta
kb.
23.1
9.4
6.6
4.3
2.3
2.0
Probe:
JH
Cα
Enzyme:
BamHI

FIG. 9B



B, *Bam*HI; H, *Hin*dIII; S, *Sac*II; X, *Xba*I; Xh, *Xho*I

chromosomal breakpoint

FIG. 10

MUM2 **Transcripts detected in MM/PCL Cell Lines**

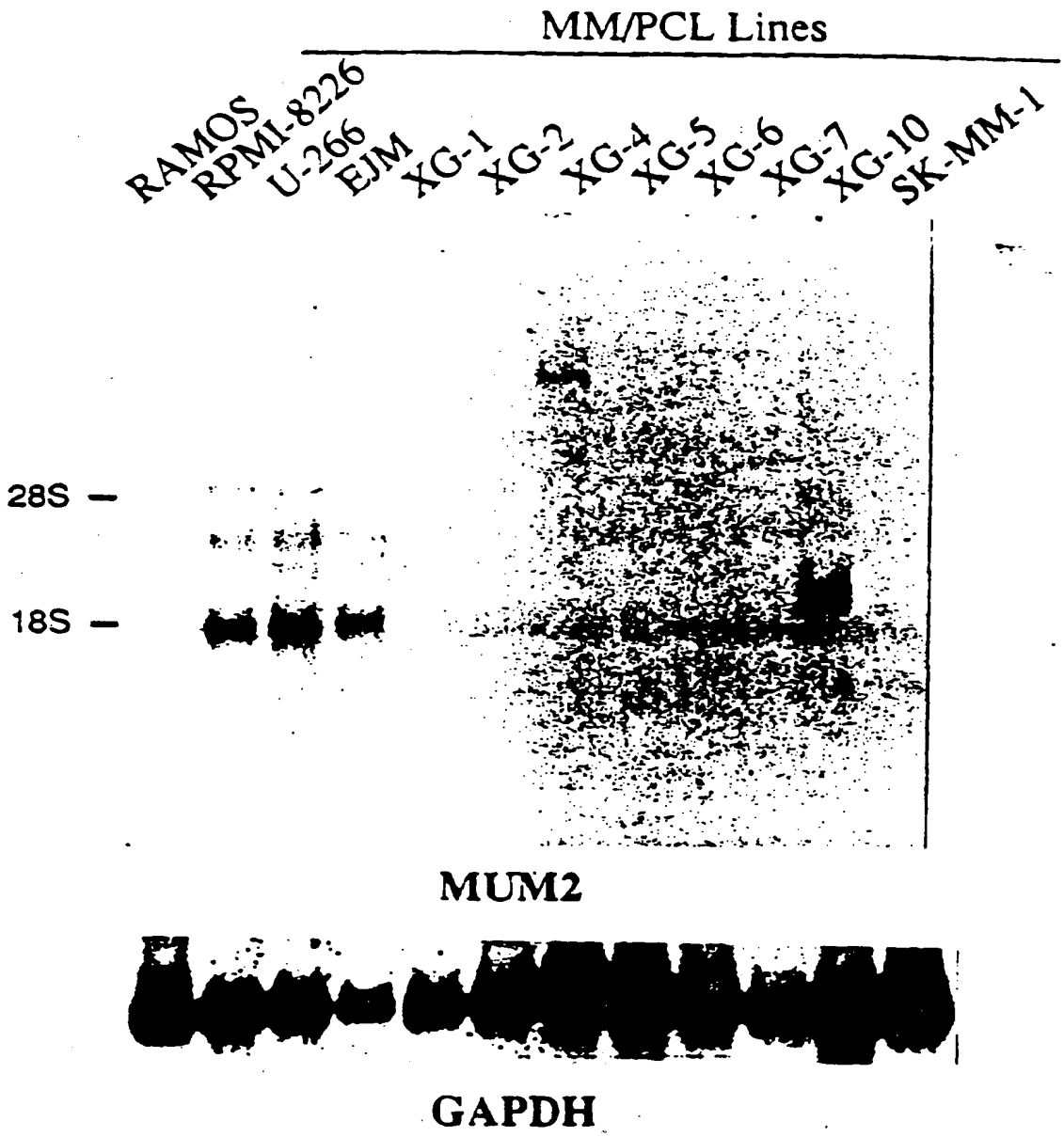


FIG. 11A

Physiological IgH gene rearrangement

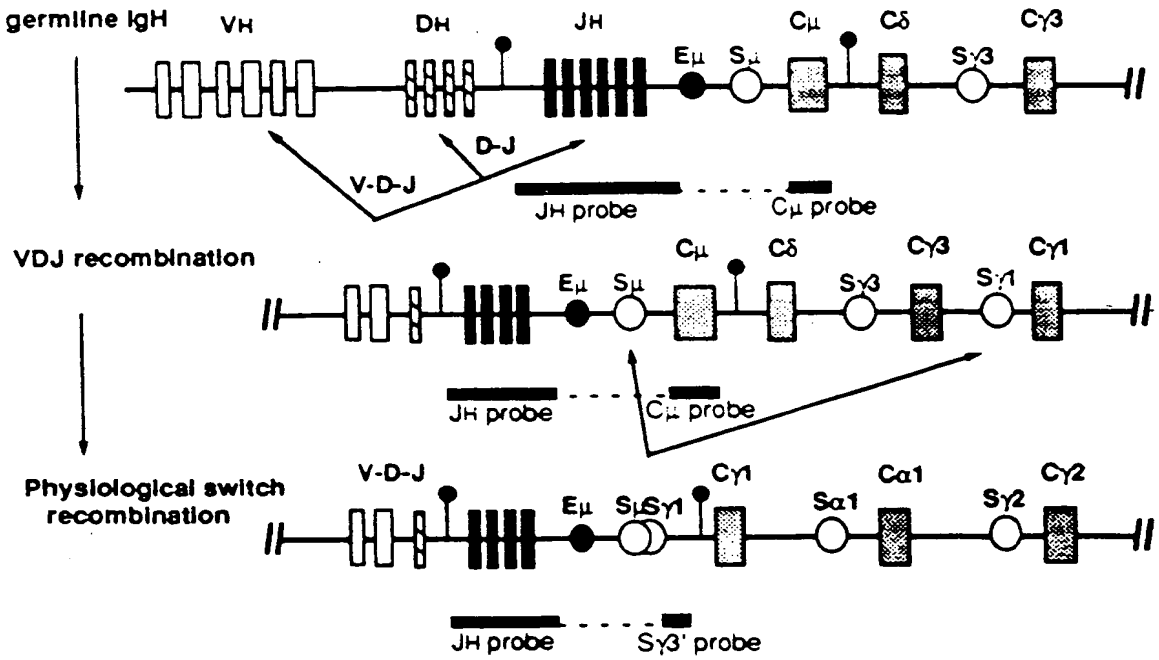
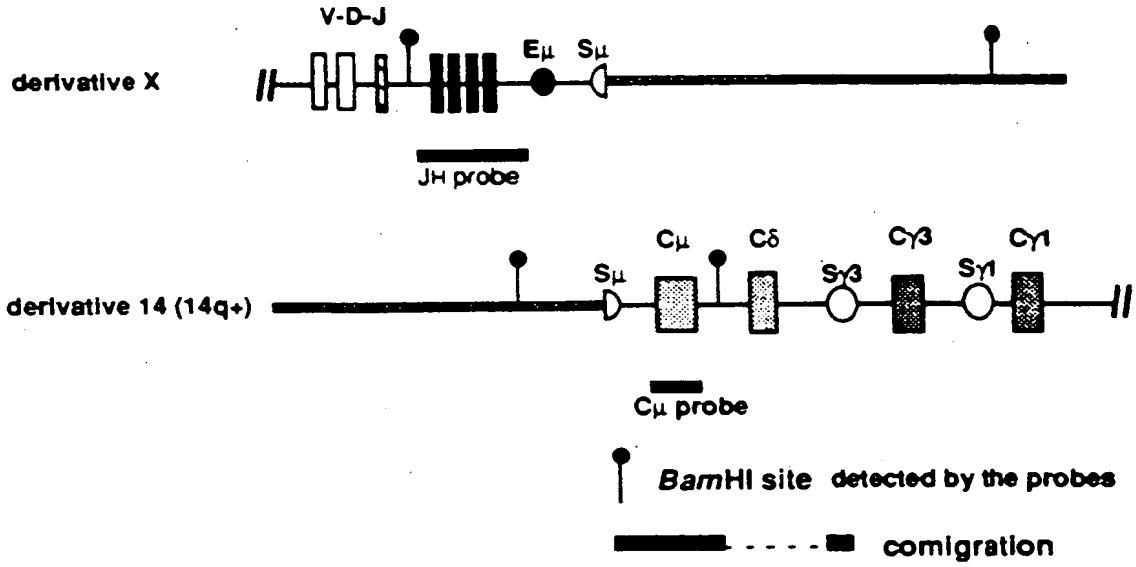
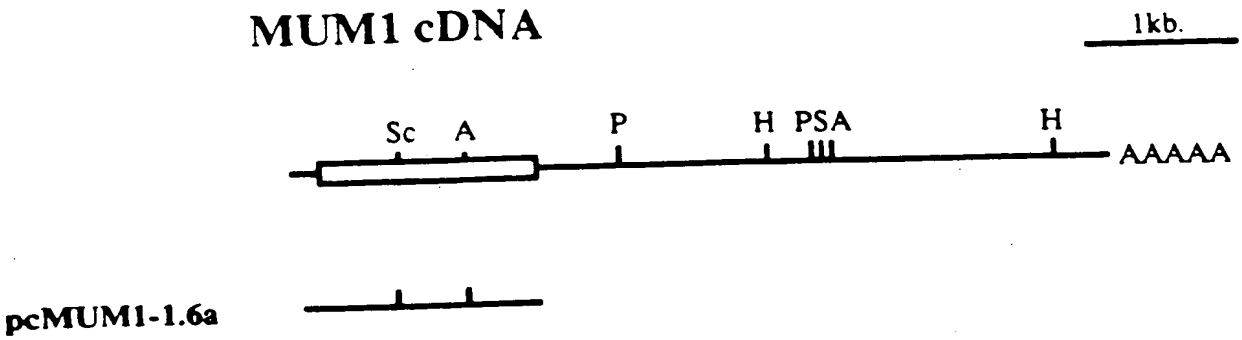


FIG. 11B

Chromosomal translocation occuring in switch region





Sc; SacII, P;*Pst*I, H;*Hin*dIII, S;*Sac*I, A;*Apa*I

cDNA inserts is cloned into EcoRI / BamHI site of the pBluescript KS+ Bacteria strain used is DH5α cells. pcMUM1-1.6a contains full length open reading frame of nt.217~1572.

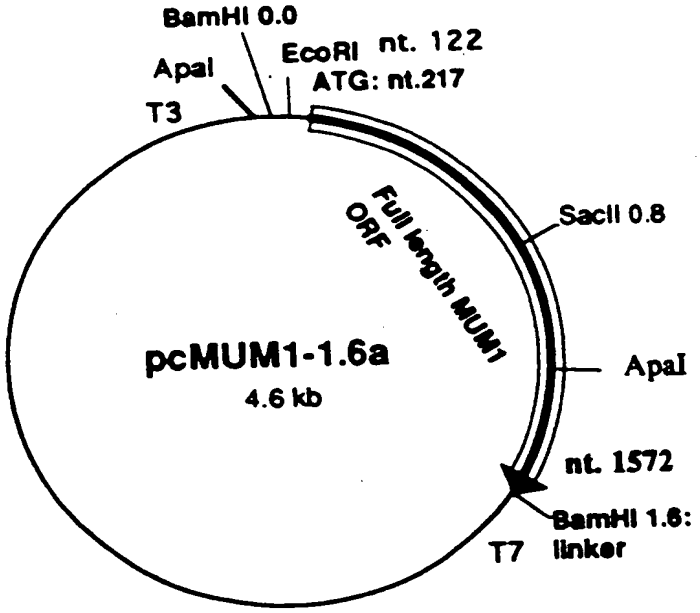
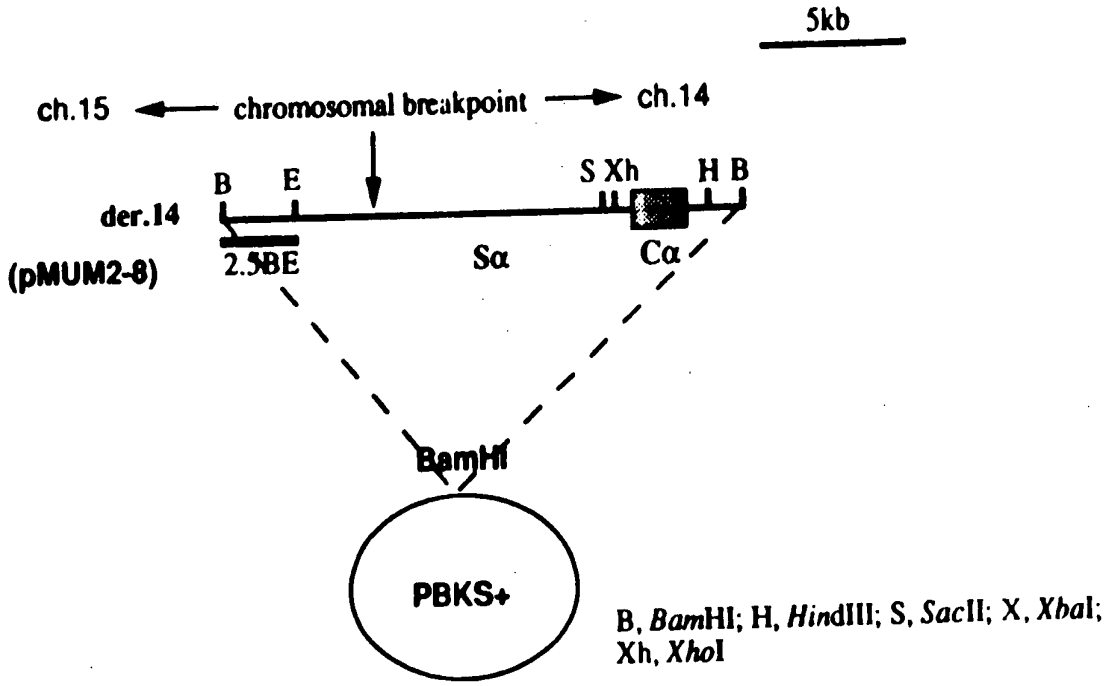


FIG. 12 A-B

Breakpoint Cloning of the U-266 Cell Line



pMUM2-8 has a 22.0kb insert in BamHI site of pBluescript KS+.

FIG. 13